# The common bean chloroplast trnH (GUG) gene and its eukaryotic putative promoter elements

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The chloroplast trnH (GUG) gene has been sequenced in several plant species, such as tobacco (1), maize (2), broad bean (3) and appears to be conserved in its nucleotide sequence during chloroplast genome evolution. This gene contains complementary sequences to two of three putative eukaryotic promoter elements. These are the CAAT box which lies in the 5′ region of the gene's 5′ exon and the GC box which is situated at the 3′ end of the gene's 3′ exon. In the various plants analysed the TATA box has not been found to lie at the expected distance; neither inside, nor upstream of the gene (tobacco, maize). In the pea and broad bean (4), which belong to the leguminous family, this TATA box lies within the expected distance from the CAAT box. Such results have not yet been indicated in the literature.

In this report, we describe the nucleotide sequence of the chloroplast trnH (GUG) gene of common bean, another leguminous plant (Figure 1). This gene shows 100% nucleotide sequence homology to its broad bean homologue. It also contains, as compared to the plants mentioned above, the complementary sequences to the CAAT and the GC boxes (underlined). But, in addition to these boxes, we have found in the 5′ region of this gene, a sequence complementary to the TATA box. We do not yet know if these sequences have any functional role in the transcription of the common bean chloroplast trnH (GUG) gene, which does not possess in its upstream region promoter sequences of chloroplast or bacterial-type (5). However, our experiments have shown that the *in vitro* transcription of this gene does not occur in the presence of *E.coli* RNA polymerase.

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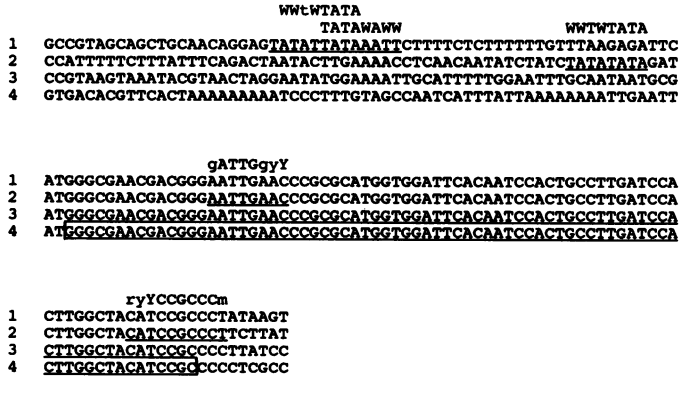


**Figure 1.** Comparison of the trnH (GUG) gene and its 5′ upstream region, in different plant species: (1) Broad bean; (2) Common bean; (3) Maize; (4) Tobacco. The eukaryotic putative sequences are underlined and the trnH (GUG) gene is boxed.